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General information about the UniProt/TrEMBL entry

Entry name

Q847D1_NODSP

Primary accession number

Q847D1

Entered in TrEMBL

Release 24, 01-JUN-2003

Sequence was last modified

Release 24, 01-JUN-2003

Annotations were last modified

Release 26, 01-MAR-2004

Protein description

Protein name

Putative beta-carotene ketolase

Origin of the protein

From

Nodularia spumigena[TaxID:70799]

Taxonomy

Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nodularia.

References

[1] NUCLEOTIDE SEQUENCE.

STRAIN=NSOR10;
DOI=10.1007/s00239-002-2415-0; MEDLINE=22549861; PubMed=12664164; [NCBI, ExPASY, EBI, Israel, Japan]
Moffitt M. C., Neilan B. A.; "Evolutionary affiliations within the superfamily of ketosynthases reflect complex pathway associations.", J. Mol. Evol. 56:446-457(2003).

[2] NUCLEOTIDE SEQUENCE.

STRAIN=NSOR10; DOI=10.1128/AEM.70.11.6353-6362.2004; PubMed=15528492; [NCBI, ExPASy, EBI, Israel, Japan]	Moffitt M.C., Neilan B.A.; "Characterization of the nodularin synthetase gene cluster and proposed theory of the evolution of cyanobacterial hepatotoxins.", Appl. Environ. Microbiol. 70:6353-6362(2004).																		
Cross-references																			
EMBL	AY210783; AAO64399.1; -; Genomic_DNA.[EMBL/ GenBank/ DDBJ] [CoDingSequence]																		
GO	<table border="1"> <tr> <td>Cellular component</td><td>membrane</td><td>GO:0016020 inferred from electronic annotation</td></tr> <tr> <td>Molecular function</td><td>oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water</td><td>GO:0016717 inferred from electronic annotation</td></tr> <tr> <td>Molecular function</td><td>oxidoreductase activity, acting on single donors with incorporation of molecular oxygen</td><td>GO:0016701 inferred from electronic annotation</td></tr> <tr> <td>Biological process</td><td>carotene metabolism</td><td>GO:0016119 inferred from electronic annotation</td></tr> <tr> <td>Biological process</td><td>fatty acid desaturation</td><td>GO:0006636 inferred from electronic annotation</td></tr> <tr> <td></td><td></td><td>[QuickGO]</td></tr> </table>	Cellular component	membrane	GO:0016020 inferred from electronic annotation	Molecular function	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	GO:0016717 inferred from electronic annotation	Molecular function	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0016701 inferred from electronic annotation	Biological process	carotene metabolism	GO:0016119 inferred from electronic annotation	Biological process	fatty acid desaturation	GO:0006636 inferred from electronic annotation			[QuickGO]
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Biological process	fatty acid desaturation	GO:0006636 inferred from electronic annotation																	
		[QuickGO]																	
InterPro	<p>IPRO011393; Carotene_ketolas.</p> <p>IPRO005804; Fa_desat.</p> <p>IPRO010257; FA_desat_sub.</p> <p>Graphical view of the domain structure</p>																		
Pfam	<p>PF00487; FA_desaturase; 1.</p> <p>Pfam graphical view of domain structure</p>																		
PIRSF	PIRSF027840; Carotene_ketolas; 1.																		
ProDom	PD001081; FA_desat_sub; 1. [Domain structure/ List of seq. sharing at least 1 domain]																		
Sequence information																			
Length	229 AA																		
Molecular weight	27832 Da																		

CRC64 71C9271BB371C95B [This is a checksum on the sequence]

MAIAIIISIVA ISLGLLLYID ISQFKWMILL PLIFWQTFLY TGLFITAHDA 50
MHGVVFPKNP KINHFIGSLC IFLYGLLPYQ KLLKKHHLHH HNPASETDPD 100
FHNGKQKNFF AWLYFMKRY WSMQITLMI IYNNLKYIW HFPEDDNTYF 150
WVVPVSISSLQ LFYFGTFLP HSEPVEGYKE PHRSOTISRP IWWFSFTCYH 200
FGYHYEHHEY PHVPMWOLPE IYKMSKSNL 229

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